

SEQUENCE LISTING

<110> Dale L. Ludwig

<120> Fully Human Antibodies Directed Against the Human Insulin-Like Growth Factor-1 Receptor

<130> 11245/53202

<140> To Be Assigned

<141> Herewith...2005-11-01

<150> PCT/US2004/013852

<151> 2004-05-03

<150> US 60/467,177

<151> 2003-05-01

<160> 33

<170> PatentIn version 3.3

<210> 1

<211> 390

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (1)..(390)

<400> 1

gag	gtc	cag	ctg	gtg	cag	tct	ggg	gct	gag	gtg	aag	aag	cct	ggg	tcc	48
Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser	
1				5					10					15		
tcg	gtg	aag	gtc	tcc	tgc	aag	gct	tct	gga	ggc	acc	ttc	agc	agc	tat	96
Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr	
			20					25					30			
gct	atc	agc	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	gag	tgg	atg	144
Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met	
		35					40					45				
gga	ggg	atc	atc	cct	atc	ttt	ggt	aca	gca	aac	tac	gca	cag	aag	ttc	192
Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe	
	50					55					60					
cag	ggc	aga	gtc	acg	att	acc	gcg	gac	aaa	tcc	acg	agc	aca	gcc	tac	240
Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr	
65					70					75					80	
atg	gag	ctg	agc	agc	ctg	aga	tct	gag	gac	acg	gcc	gtg	tat	tac	tgt	288
Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	
				85				90					95			
gcg	aga	gcg	cca	tta	cga	ttt	ttg	gag	tgg	tcc	acc	caa	gac	cac	tac	336
Ala	Arg	Ala	Pro	Leu	Arg	Phe	Leu	Glu	Trp	Ser	Thr	Gln	Asp	His	Tyr	
			100					105					110			

tac	tac	tac	tac	atg	gac	gtc	tgg	ggc	aaa	ggg	acc	acg	gtc	acc	gtc	384
Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val	
		115					120					125				

tca	agc	390
Ser	Ser	
	130	

<210> 2  
 <211> 130  
 <212> PRT  
 <213> Homo sapiens

<400> 2

Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	Pro	Gly	Ser
1				5					10					15	

Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	Ser	Ser	Tyr
			20					25					30		

Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	Glu	Trp	Met
		35					40					45			

Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	Gln	Lys	Phe
	50					55					60				

Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	Thr	Ala	Tyr
65					70					75					80

Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys
				85					90					95	

Ala	Arg	Ala	Pro	Leu	Arg	Phe	Leu	Glu	Trp	Ser	Thr	Gln	Asp	His	Tyr
			100					105					110		

Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	Val	Thr	Val
		115					120					125			

Ser	Ser
	130

<210> 3  
 <211> 1440  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1) .. (1440)

<400> 3																
atg	gga	tgg	tca	tgt	atc	atc	ctt	ttt	cta	gta	gca	act	gca	act	gga	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1 5 10 15																
gta	cat	tca	gag	gtc	cag	ctg	gtg	cag	tct	ggg	gct	gag	gtg	aag	aag	96
Val	His	Ser	Glu	Val	Gln	Leu	Val	Gln	Ser	Gly	Ala	Glu	Val	Lys	Lys	
20 25 30																
cct	ggg	tcc	tcg	gtg	aag	gtc	tcc	tgc	aag	gct	tct	gga	ggc	acc	ttc	144
Pro	Gly	Ser	Ser	Val	Lys	Val	Ser	Cys	Lys	Ala	Ser	Gly	Gly	Thr	Phe	
35 40 45																
agc	agc	tat	gct	atc	agc	tgg	gtg	cga	cag	gcc	cct	gga	caa	ggg	ctt	192
Ser	Ser	Tyr	Ala	Ile	Ser	Trp	Val	Arg	Gln	Ala	Pro	Gly	Gln	Gly	Leu	
50 55 60																
gag	tgg	atg	gga	ggg	atc	atc	cct	atc	ttt	ggg	aca	gca	aac	tac	gca	240
Glu	Trp	Met	Gly	Gly	Ile	Ile	Pro	Ile	Phe	Gly	Thr	Ala	Asn	Tyr	Ala	
65 70 75 80																
cag	aag	ttc	cag	ggc	aga	gtc	acg	att	acc	gcg	gac	aaa	tcc	acg	agc	288
Gln	Lys	Phe	Gln	Gly	Arg	Val	Thr	Ile	Thr	Ala	Asp	Lys	Ser	Thr	Ser	
85 90 95																
aca	gcc	tac	atg	gag	ctg	agc	agc	ctg	aga	tct	gag	gac	acg	gcc	gtg	336
Thr	Ala	Tyr	Met	Glu	Leu	Ser	Ser	Leu	Arg	Ser	Glu	Asp	Thr	Ala	Val	
100 105 110																
tat	tac	tgt	gcg	aga	gcg	cca	tta	cga	ttt	ttg	gag	tgg	tcc	acc	caa	384
Tyr	Tyr	Cys	Ala	Arg	Ala	Pro	Leu	Arg	Phe	Leu	Glu	Trp	Ser	Thr	Gln	
115 120 125																
gac	cac	tac	tac	tac	tac	tac	atg	gac	gtc	tgg	ggc	aaa	ggg	acc	acg	432
Asp	His	Tyr	Tyr	Tyr	Tyr	Tyr	Met	Asp	Val	Trp	Gly	Lys	Gly	Thr	Thr	
130 135 140																
gtc	acc	gtc	tca	agc	gcc	tcc	acc	aag	ggc	cca	tcg	gtc	ttc	ccc	ctg	480
Val	Thr	Val	Ser	Ser	Ala	Ser	Thr	Lys	Gly	Pro	Ser	Val	Phe	Pro	Leu	
145 150 155 160																
gca	ccc	tcc	tcc	aag	agc	acc	tct	ggg	ggc	aca	gcg	gcc	ctg	ggc	tgc	528
Ala	Pro	Ser	Ser	Lys	Ser	Thr	Ser	Gly	Gly	Thr	Ala	Ala	Leu	Gly	Cys	
165 170 175																
ctg	gtc	aag	gac	tac	ttc	ccc	gaa	ccg	gtg	acg	gtg	tcg	tgg	aac	tca	576
Leu	Val	Lys	Asp	Tyr	Phe	Pro	Glu	Pro	Val	Thr	Val	Ser	Trp	Asn	Ser	
180 185 190																
ggc	gcc	ctg	acc	agc	ggc	gtg	cac	acc	ttc	ccg	gct	gtc	cta	cag	tcc	624
Gly	Ala	Leu	Thr	Ser	Gly	Val	His	Thr	Phe	Pro	Ala	Val	Leu	Gln	Ser	
195 200 205																
tca	gga	ctc	tac	tcc	ctc	agc	agc	gtg	gtg	acc	gtg	ccc	tcc	agc	agc	672
Ser	Gly	Leu	Tyr	Ser	Leu	Ser	Ser	Val	Val	Thr	Val	Pro	Ser	Ser	Ser	
210 215 220																
ttg	ggc	acc	cag	acc	tac	atc	tgc	aac	gtg	aat	cac	aag	ccc	agc	aac	720
Leu	Gly	Thr	Gln	Thr	Tyr	Ile	Cys	Asn	Val	Asn	His	Lys	Pro	Ser	Asn	
225 230 235 240																

acc aag gtg gac aag aaa gtt gag ccc aaa tct tgt gac aaa act cac	768
Thr Lys Val Asp Lys Lys Val Glu Pro Lys Ser Cys Asp Lys Thr His	
245 250 255	
aca tgc cca ccg tgc cca gca cct gaa ctc ctg ggg gga ccg tca gtc	816
Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly Gly Pro Ser Val	
260 265 270	
ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg atc tcc cgg acc	864
Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met Ile Ser Arg Thr	
275 280 285	
cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac gaa gac cct gag	912
Pro Glu Val Thr Cys Val Val Val Asp Val Ser His Glu Asp Pro Glu	
290 295 300	
gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg cat aat gcc aag	960
Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val His Asn Ala Lys	
305 310 315 320	
aca aag ccg cgg gag gag cag tac aac agc acg tac cgg gtg gtc agc	1008
Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr Arg Val Val Ser	
325 330 335	
gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc aag gag tac aag	1056
Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys	
340 345 350	
tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc gag aaa acc atc	1104
Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile	
355 360 365	
tcc aaa gcc aaa ggg cag ccc cga gaa cca cag gtg tac acc ctg ccc	1152
Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro	
370 375 380	
cca tcc ccg gag gag atg acc aag aac cag gtc agc ctg acc tgc ctg	1200
Pro Ser Arg Glu Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu	
385 390 395 400	
gtc aaa ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat	1248
Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn	
405 410 415	
ggg cag ccg gag aac aac tac aag acc acg cct ccc gtg ctg gac tcc	1296
Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser	
420 425 430	
gac ggc tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg	1344
Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg	
435 440 445	
tgg cag cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg	1392
Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu	
450 455 460	
cac aac cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	1440
His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys	
465 470 475	

<210> 4  
<211> 479  
<212> PRT  
<213> Homo sapiens

<400> 4

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Glu Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys  
20 25 30

Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Gly Thr Phe  
35 40 45

Ser Ser Tyr Ala Ile Ser Trp Val Arg Gln Ala Pro Gly Gln Gly Leu  
50 55 60

Glu Trp Met Gly Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala  
65 70 75 80

Gln Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Lys Ser Thr Ser  
85 90 95

Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Val  
100 105 110

Tyr Tyr Cys Ala Arg Ala Pro Leu Arg Phe Leu Glu Trp Ser Thr Gln  
115 120 125

Asp His Tyr Tyr Tyr Tyr Tyr Met Asp Val Trp Gly Lys Gly Thr Thr  
130 135 140

Val Thr Val Ser Ser Ala Ser Thr Lys Gly Pro Ser Val Phe Pro Leu  
145 150 155 160

Ala Pro Ser Ser Lys Ser Thr Ser Gly Gly Thr Ala Ala Leu Gly Cys  
165 170 175

Leu Val Lys Asp Tyr Phe Pro Glu Pro Val Thr Val Ser Trp Asn Ser  
180 185 190

Gly Ala Leu Thr Ser Gly Val His Thr Phe Pro Ala Val Leu Gln Ser  
195 200 205

Ser Gly Leu Tyr Ser Leu Ser Ser Val Val Thr Val Pro Ser Ser Ser

210	215	220														
Leu 225	Gly	Thr	Gln	Thr	Tyr 230	Ile	Cys	Asn	Val	Asn 235	His	Lys	Pro	Ser	Asn 240	
Thr	Lys	Val	Asp	Lys 245	Lys	Val	Glu	Pro	Lys 250	Ser	Cys	Asp	Lys	Thr	His 255	
Thr	Cys	Pro	Pro 260	Cys	Pro	Ala	Pro	Glu 265	Leu	Leu	Gly	Gly	Pro	Ser	Val 270	
Phe	Leu	Phe 275	Pro	Pro	Lys	Pro	Lys 280	Asp	Thr	Leu	Met	Ile 285	Ser	Arg	Thr	
Pro	Glu 290	Val	Thr	Cys	Val	Val 295	Val	Asp	Val	Ser	His 300	Glu	Asp	Pro	Glu	
Val 305	Lys	Phe	Asn	Trp	Tyr 310	Val	Asp	Gly	Val	Glu 315	Val	His	Asn	Ala	Lys 320	
Thr	Lys	Pro	Arg	Glu 325	Glu	Gln	Tyr	Asn	Ser 330	Thr	Tyr	Arg	Val	Val 335	Ser	
Val	Leu	Thr	Val 340	Leu	His	Gln	Asp	Trp 345	Leu	Asn	Gly	Lys	Glu 350	Tyr	Lys	
Cys	Lys	Val 355	Ser	Asn	Lys	Ala	Leu 360	Pro	Ala	Pro	Ile	Glu 365	Lys	Thr	Ile	
Ser 370	Lys	Ala	Lys	Gly	Gln	Pro 375	Arg	Glu	Pro	Gln	Val 380	Tyr	Thr	Leu	Pro	
Pro 385	Ser	Arg	Glu	Glu	Met 390	Thr	Lys	Asn	Gln	Val 395	Ser	Leu	Thr	Cys	Leu 400	
Val	Lys	Gly	Phe	Tyr 405	Pro	Ser	Asp	Ile	Ala 410	Val	Glu	Trp	Glu	Ser	Asn 415	
Gly	Gln	Pro	Glu 420	Asn	Asn	Tyr	Lys	Thr 425	Thr	Pro	Pro	Val	Leu 430	Asp	Ser	
Asp	Gly	Ser	Phe	Phe	Leu	Tyr	Ser 440	Lys	Leu	Thr	Val	Asp 445	Lys	Ser	Arg	
Trp 450	Gln	Gln	Gly	Asn	Val	Phe 455	Ser	Cys	Ser	Val	Met 460	His	Glu	Ala	Leu	

His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly Lys  
 465 470 475

<210> 5  
 <211> 327  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(327)

<400> 5  
 tct tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag 48  
 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln  
 1 5 10 15  
 aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96  
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala  
 20 25 30  
 agc tgg tac cag cag aag cca gga cag gcc cct gta ctt gtc atc tat 144  
 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
 35 40 45  
 ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192  
 Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser  
 50 55 60  
 agc tca gga aac aca gct tcc ttg acc atc act ggg gct cag gcg gaa 240  
 Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu  
 65 70 75 80  
 gat gag gct gac tat tac tgt aac tcc cgg gac aac agt gat aac cgt 288  
 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser Asp Asn Arg  
 85 90 95  
 ctg ata ttt ggc ggc ggg acc aag ctg acc gtc ctc agt 327  
 Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser  
 100 105

<210> 6  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 6  
 Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln  
 1 5 10 15  
 Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala  
 20 25 30

Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu Val Ile Tyr  
35 40 45

Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe Ser Gly Ser  
50 55 60

Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala Gln Ala Glu  
65 70 75 80

Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser Asp Asn Arg  
85 90 95

Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser  
100 105

<210> 7  
<211> 702  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(702)

<400> 7  
atg gga tgg tca tgt atc atc ctt ttt cta gta gca act gca act gga 48  
Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15  
gta cat tca tct tct gag ctg act cag gac cct gct gtg tct gtg gcc 96  
Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala  
20 25 30  
ttg gga cag aca gtc agg atc aca tgc caa gga gac agc ctc aga agc 144  
Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser  
35 40 45  
tat tat gca agc tgg tac cag cag aag cca gga cag gcc cct gta ctt 192  
Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu  
50 55 60  
gtc atc tat ggt aaa aac aac cgg ccc tca ggg atc cca gac cga ttc 240  
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe  
65 70 75 80  
tct ggc tcc agc tca gga aac aca gct tcc ttg acc atc act ggg gct 288  
Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala  
85 90 95  
cag gcg gaa gat gag gct gac tat tac tgt aac tcc cgg gac aac agt 336  
Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser  
100 105 110  
gat aac cgt ctg ata ttt ggc ggc ggg acc aag ctg acc gtc ctc agt 384  
Asp Asn Arg Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser



115	120	125	
cag ccc aag gct gcc ccc tcg gtc act ctg ttc ccg ccc tcc tct gag Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu 130 135 140			432
gag ctt caa gcc aac aag gcc aca ctg gtg tgt ctc ata agt gac ttc Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe 145 150 155 160			480
tac ccg gga gcc gtg aca gtg gcc tgg aag gca gat agc agc ccc gtc Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val 165 170 175			528
aag gcg gga gtg gag acc acc aca ccc tcc aaa caa agc aac aac aag Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys 180 185 190			576
tac gcg gcc agc agc tat ctg agc ctg acg cct gag cag tgg aag tcc Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser 195 200 205			624
cac aga agc tac agc tgc cag gtc acg cat gaa ggg agc acc gtg gag His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu 210 215 220			672
aag aca gtg gcc cct gca gaa tgc tct tga Lys Thr Val Ala Pro Ala Glu Cys Ser 225 230			702

<210> 8  
 <211> 233  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly 1 5 10 15
Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala 20 25 30
Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser 35 40 45
Tyr Tyr Ala Ser Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Val Leu 50 55 60
Val Ile Tyr Gly Lys Asn Asn Arg Pro Ser Gly Ile Pro Asp Arg Phe 65 70 75 80
Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala 85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Arg Asp Asn Ser  
100 105 110

Asp Asn Arg Leu Ile Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Ser  
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu  
210 215 220

Lys Thr Val Ala Pro Ala Glu Cys Ser  
225 230

<210> 9  
<211> 327  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(327)

<400> 9  
tct tct gag ctg act cag gac cct gct gtg tct gtg gcc ttg gga cag 48  
Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala Leu Gly Gln  
1 5 10 15  
aca gtc agg atc aca tgc caa gga gac agc ctc aga agc tat tat gca 96  
Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala  
20 25 30  
acc tgg tac cag cag aag cca gga cag gcc cct att ctt gtc atc tat 144  
Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu Val Ile Tyr  
35 40 45  
ggt gaa aat aag cgg ccc tca ggg atc cca gac cga ttc tct ggc tcc 192

Gly	Glu	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
50						55					60						
agc	tca	gga	aac	aca	gct	tcc	ttg	acc	atc	act	ggg	gct	cag	gca	gaa		240
Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu		
65					70					75					80		
gat	gag	gct	gac	tac	tat	tgt	aaa	tct	cgg	gat	ggc	agt	ggt	caa	cat		288
Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Lys	Ser	Arg	Asp	Gly	Ser	Gly	Gln	His		
				85					90					95			
ctg	gtg	ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	ggt					327
Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly					
			100					105									

<210> 10  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	Leu	Gly	Gln		
1				5					10					15			

Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	Tyr	Tyr	Ala		
			20					25					30				

Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Ile	Leu	Val	Ile	Tyr		
		35					40					45					

Gly	Glu	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	Ser	Gly	Ser		
50						55					60						

Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	Gln	Ala	Glu		
65					70					75					80		

Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Lys	Ser	Arg	Asp	Gly	Ser	Gly	Gln	His		
				85					90					95			

Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly					
			100					105									

<210> 11  
 <211> 702  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> CDS  
 <222> (1)..(702)

<400>	11															
atg	gga	tgg	tca	tgt	atc	atc	ctt	ttt	cta	gta	gca	act	gca	act	gga	48
Met	Gly	Trp	Ser	Cys	Ile	Ile	Leu	Phe	Leu	Val	Ala	Thr	Ala	Thr	Gly	
1				5					10					15		
gta	cat	tca	tct	tct	gag	ctg	act	cag	gac	cct	gct	gtg	tct	gtg	gcc	96
Val	His	Ser	Ser	Ser	Glu	Leu	Thr	Gln	Asp	Pro	Ala	Val	Ser	Val	Ala	
			20					25					30			
ttg	gga	cag	aca	gtc	agg	atc	aca	tgc	caa	gga	gac	agc	ctc	aga	agc	144
Leu	Gly	Gln	Thr	Val	Arg	Ile	Thr	Cys	Gln	Gly	Asp	Ser	Leu	Arg	Ser	
		35					40					45				
tat	tat	gca	acc	tgg	tac	cag	cag	aag	cca	gga	cag	gcc	cct	att	ctt	192
Tyr	Tyr	Ala	Thr	Trp	Tyr	Gln	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Ile	Leu	
	50					55					60					
gtc	atc	tat	ggg	gaa	aat	aag	cgg	ccc	tca	ggg	atc	cca	gac	cga	ttc	240
Val	Ile	Tyr	Gly	Glu	Asn	Lys	Arg	Pro	Ser	Gly	Ile	Pro	Asp	Arg	Phe	
65					70					75					80	
tct	ggc	tcc	agc	tca	gga	aac	aca	gct	tcc	ttg	acc	atc	act	ggg	gct	288
Ser	Gly	Ser	Ser	Ser	Gly	Asn	Thr	Ala	Ser	Leu	Thr	Ile	Thr	Gly	Ala	
				85					90					95		
cag	gca	gaa	gat	gag	gct	gac	tac	tat	tgt	aaa	tct	cgg	gat	ggc	agt	336
Gln	Ala	Glu	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Lys	Ser	Arg	Asp	Gly	Ser	
			100					105					110			
ggg	caa	cat	ctg	gtg	ttc	ggc	gga	ggg	acc	aag	ctg	acc	gtc	cta	ggg	384
Gly	Gln	His	Leu	Val	Phe	Gly	Gly	Gly	Thr	Lys	Leu	Thr	Val	Leu	Gly	
		115					120					125				
cag	ccc	aag	gct	gcc	ccc	tcg	gtc	act	ctg	ttc	ccg	ccc	tcc	tct	gag	432
Gln	Pro	Lys	Ala	Ala	Pro	Ser	Val	Thr	Leu	Phe	Pro	Pro	Ser	Ser	Glu	
	130					135					140					
gag	ctt	caa	gcc	aac	aag	gcc	aca	ctg	gtg	tgt	ctc	ata	agt	gac	ttc	480
Glu	Leu	Gln	Ala	Asn	Lys	Ala	Thr	Leu	Val	Cys	Leu	Ile	Ser	Asp	Phe	
145					150					155					160	
tac	ccg	gga	gcc	gtg	aca	gtg	gcc	tgg	aag	gca	gat	agc	agc	ccc	gtc	528
Tyr	Pro	Gly	Ala	Val	Thr	Val	Ala	Trp	Lys	Ala	Asp	Ser	Ser	Pro	Val	
				165					170					175		
aag	gcg	gga	gtg	gag	acc	acc	aca	ccc	tcc	aaa	caa	agc	aac	aac	aag	576
Lys	Ala	Gly	Val	Glu	Thr	Thr	Thr	Pro	Ser	Lys	Gln	Ser	Asn	Asn	Lys	
			180					185					190			
tac	gcg	gcc	agc	agc	tat	ctg	agc	ctg	acg	cct	gag	cag	tgg	aag	tcc	624
Tyr	Ala	Ala	Ser	Ser	Tyr	Leu	Ser	Leu	Thr	Pro	Glu	Gln	Trp	Lys	Ser	

<210> 12  
<211> 233  
<212> PRT  
<213> Homo sapiens

<400> 12

Met Gly Trp Ser Cys Ile Ile Leu Phe Leu Val Ala Thr Ala Thr Gly  
1 5 10 15

Val His Ser Ser Ser Glu Leu Thr Gln Asp Pro Ala Val Ser Val Ala  
20 25 30

Leu Gly Gln Thr Val Arg Ile Thr Cys Gln Gly Asp Ser Leu Arg Ser  
35 40 45

Tyr Tyr Ala Thr Trp Tyr Gln Gln Lys Pro Gly Gln Ala Pro Ile Leu  
50 55 60

Val Ile Tyr Gly Glu Asn Lys Arg Pro Ser Gly Ile Pro Asp Arg Phe  
65 70 75 80

Ser Gly Ser Ser Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Gly Ala  
85 90 95

Gln Ala Glu Asp Glu Ala Asp Tyr Tyr Cys Lys Ser Arg Asp Gly Ser  
100 105 110

Gly Gln His Leu Val Phe Gly Gly Gly Thr Lys Leu Thr Val Leu Gly  
115 120 125

Gln Pro Lys Ala Ala Pro Ser Val Thr Leu Phe Pro Pro Ser Ser Glu  
130 135 140

Glu Leu Gln Ala Asn Lys Ala Thr Leu Val Cys Leu Ile Ser Asp Phe  
145 150 155 160

Tyr Pro Gly Ala Val Thr Val Ala Trp Lys Ala Asp Ser Ser Pro Val  
165 170 175

Lys Ala Gly Val Glu Thr Thr Thr Pro Ser Lys Gln Ser Asn Asn Lys  
180 185 190

Tyr Ala Ala Ser Ser Tyr Leu Ser Leu Thr Pro Glu Gln Trp Lys Ser  
195 200 205

His Arg Ser Tyr Ser Cys Gln Val Thr His Glu Gly Ser Thr Val Glu

210	215	220
Lys Thr Val Ala Pro Ala Glu Cys Ser		
225	230	
<210> 13		
<211> 15		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> CDS		
<222> (1)..(15)		
<400> 13		
agc tat gct atc agc		15
Ser Tyr Ala Ile Ser		
1 5		
<210> 14		
<211> 5		
<212> PRT		
<213> Homo sapiens		
<400> 14		
Ser Tyr Ala Ile Ser		
1 5		
<210> 15		
<211> 51		
<212> DNA		
<213> Homo sapiens		
<220>		
<221> CDS		
<222> (1)..(51)		
<400> 15		
ggg atc atc cct atc ttt ggt aca gca aac tac gca cag aag ttc cag		48
Gly Ile Ile Pro Ile Phe Gly Thr Ala Asn Tyr Ala Gln Lys Phe Gln		
1 5 10 15		
ggc		51
Gly		
<210> 16		
<211> 17		
<212> PRT		
<213> Homo sapiens		
<400> 16		



<212> PRT  
<213> Homo sapiens

<400> 20

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Ser  
1 5 10

<210> 21  
<211> 21  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(21)

<400> 21  
ggt aaa aac aac cgg ccc tca  
Gly Lys Asn Asn Arg Pro Ser  
1 5

21

<210> 22  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 22

Gly Lys Asn Asn Arg Pro Ser  
1 5

<210> 23  
<211> 33  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(33)

<400> 23  
aac tcc cgg gac aac agt gat aac cgt ctg ata  
Asn Ser Arg Asp Asn Ser Asp Asn Arg Leu Ile  
1 5 10

33

<210> 24  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 24

Asn Ser Arg Asp Asn Ser Asp Asn Arg Leu Ile  
1 5 10



<210> 25  
<211> 33  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) .. (33)

<400> 25  
caa gga gac agc ctc aga agc tat tat gca acc  
Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Thr  
1 5 10

33

<210> 26  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 26

Gln Gly Asp Ser Leu Arg Ser Tyr Tyr Ala Thr  
1 5 10

<210> 27  
<211> 21  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1) .. (21)

<400> 27  
ggt gaa aat aag cgg ccc tca  
Gly Glu Asn Lys Arg Pro Ser  
1 5

21

<210> 28  
<211> 7  
<212> PRT  
<213> Homo sapiens

<400> 28

Gly Glu Asn Lys Arg Pro Ser  
1 5

<210> 29  
<211> 33  
<212> DNA  
<213> Homo sapiens

<220>  
<221> CDS  
<222> (1)..(33)

<400> 29  
aaa tct cgg gat ggc agt ggt caa cat ctg gtg  
Lys Ser Arg Asp Gly Ser Gly Gln His Leu Val  
1 5 10

33

<210> 30  
<211> 11  
<212> PRT  
<213> Homo sapiens

<400> 30  
Lys Ser Arg Asp Gly Ser Gly Gln His Leu Val  
1 5 10

<210> 31  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<223> synthetic primer

<400> 31  
agcggataac aatttcacac agg

23

<210> 32  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<223> Synthetic primer

<400> 32  
gtcgtctttc cagacgtag t

21

<210> 33  
<211> 15  
<212> PRT  
<213> Artificial

<220>  
<223> peptide linker

<400> 33  
Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser  
1 5 10 15